

SEQUENCE LISTING

<110> Mahajan, Pramod B.
Shi, Jinrui

<120> Maize Rad50 Orthologue and Uses Thereof

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acc gtt gac	aag atg ctg	atc aag ggg	att cgg agc	ttc gat ccg	gac	345
Thr Val Asp	Lys Met Leu	Ile Lys Gly	Ile Arg Ser	Phe Asp Pro	Asp	
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Asn Lys Asn	Val Ile Thr	Phe Phe Lys	Pro Leu Thr	Leu Ile Val	Gly	
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ccc aac ggt	gct ggc aag	acc acg atc	atc gag tgc	ctg aag ctt	tct	441
Pro Asn Gly	Ala Gly Lys	Thr Thr Ile	Ile Glu Cys	Leu Lys Leu	Ser	
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tgc acc ggc	gag ctg ccc	ccc aac tcc	cgc tct ggc	cac acc ttc	gtc	489
Cys Thr Gly	Glu Leu Pro	Pro Asn Ser	Arg Ser Gly	His Thr Phe	Val	
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cac gac ccc	aag gta gct	ggc gag acg	gaa aca aaa	gga caa att	aag	537
His Asp Pro	Lys Val Ala	Gly Glu Thr	Glu Thr Lys	Gly Gln Ile	Lys	
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ttg cgg ttt	aag act gca	gca gga aag	gat gtg gtg	tgc atc cgg	tcc	585
Leu Arg Phe	Lys Thr Ala	Ala Gly Lys	Asp Val Val	Cys Ile Arg	Ser	
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ttc cag ctt	acc caa aag	gca tca aag	atg gag ttt	aag gca att	gaa	633
Phe Gln Leu	Thr Gln Lys	Ala Ser Lys	Met Glu Phe	Lys Ala Ile	Glu	

006220" 96282960

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agc tac aga tgt gct gac atg gat aga gag att cct gcc tta atg ggt Ser Tyr Arg Cys Ala Asp Met Asp Arg Glu Ile Pro Ala Leu Met Gly 135 140 145			729
gtt tcg aag gcc gta ctg gag aat gtt ata ttt gtt cac caa gat gaa Val Ser Lys Ala Val Leu Glu Asn Val Ile Phe Val His Gln Asp Glu 150 155 160			777
tcc aat tgg cca ttg cag gac ccg tca aca ctt aag aag aag ttc gat Ser Asn Trp Pro Leu Gln Asp Pro Ser Thr Leu Lys Lys Lys Phe Asp 165 170 175			825
gac atc ttc tct gcc aca cgc tat acg aaa gct ctt gaa gtc ata aag Asp Ile Phe Ser Ala Thr Arg Tyr Thr Lys Ala Leu Glu Val Ile Lys 180 185 190			873
aaa ctt cac aag gat caa atg caa gag atc aag act ttt agg tta aag Lys Leu His Lys Asp Gln Met Gln Glu Ile Lys Thr Phe Arg Leu Lys 195 200 205 210			921
ctg gag aac ctt cag act gta aaa gac caa gca cat aag ctg cgt gaa Leu Glu Asn Leu Gln Thr Val Lys Asp Gln Ala His Lys Leu Arg Glu 215 220 225			969
aat att gct caa gat caa gaa aag tca gat gcc tca aaa tct cag atg Asn Ile Ala Gln Asp Gln Glu Lys Ser Asp Ala Ser Lys Ser Gln Met 230 235 240			1017
gag caa ctg aag gaa aag atc tgt ggt acc gag aga gaa atc ctg caa Glu Gln Leu Lys Glu Lys Ile Cys Gly Thr Glu Arg Glu Ile Leu Gln 245 250 255			1065
atg gaa aca agt ttg gat gaa ctg aga aga ctt cag gga caa att gac Met Glu Thr Ser Leu Asp Glu Leu Arg Arg Leu Gln Gly Gln Ile Asp 260 265 270			1113
atc aag gca aca gag aga agt aca tta ctt acg cag cag cat gaa aag Ile Lys Ala Thr Glu Arg Ser Thr Leu Leu Thr Gln Gln His Glu Lys 275 280 285 290			1161
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gtt ctg tcc aaa caa aat tct gaa tta aca cat gaa att gga aag ctc Val Leu Ser Lys Gln Asn Ser Glu Leu Thr His Glu Ile Gly Lys Leu 340 345 350			1353

00538396 032900

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Gln Ala Glu Ala Asp Ala His Leu Thr Met Lys His Glu Arg Asp Ser	
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gac ata aaa aat ata tgc act aaa cat aat ctt ggg ccg gtt cct gaa	1449
Asp Ile Lys Asn Ile Cys Thr Lys His Asn Leu Gly Pro Val Pro Glu	
375 380 385	
cat ccc ttt acg aat gat gtt gct atg aac ctt aca aac agg att aaa	1497
His Pro Phe Thr Asn Asp Val Ala Met Asn Leu Thr Asn Arg Ile Lys	
390 395 400	
gcg aga cta tca agt ctt gag aat gat ttg ctg gat aag aag aaa tcc	1545
Ala Arg Leu Ser Ser Leu Glu Asn Asp Leu Leu Asp Lys Lys Lys Ser	
405 410 415	
aat gaa gat cag tta gat gtt ttg tgg aaa cac tat ctt aaa ata aat	1593
Asn Glu Asp Gln Leu Asp Val Leu Trp Lys His Tyr Leu Lys Ile Asn	
420 425 430	
gct cgc tac tcc gaa gtt gat ggt cag ata caa tct aag att gaa tcc	1641
Ala Arg Tyr Ser Glu Val Asp Gly Gln Ile Gln Ser Lys Ile Glu Ser	
435 440 445 450	
atg tca ggc att tta aga cgg aga aaa gat aaa gag aaa gaa cgc gat	1689
Met Ser Gly Ile Leu Arg Arg Arg Lys Asp Lys Glu Lys Glu Arg Asp	
455 460 465	
gct gca gaa gtg gag ctt tca aaa ttt aat cta tcc cgt atc gat gag	1737
Ala Ala Glu Val Glu Leu Ser Lys Phe Asn Leu Ser Arg Ile Asp Glu	
470 475 480	
agg gag aga cat atg caa att gaa gtc gag agg aag aca ctt gcg ctt	1785
Arg Glu Arg His Met Gln Ile Glu Val Glu Arg Lys Thr Leu Ala Leu	
485 490 495	
gga gaa aga gac tat gat tca att ata agt cag aaa cga aca gaa gta	1833
Gly Glu Arg Asp Tyr Asp Ser Ile Ile Ser Gln Lys Arg Thr Glu Val	
500 505 510	
tat agt ttg gaa cag aaa ata aaa gtg ctt ctg cgg gag aaa gat ata	1881
Tyr Ser Leu Glu Gln Lys Ile Lys Val Leu Leu Arg Glu Lys Asp Ile	
515 520 525 530	
ata aat aga aat gct gat gaa aga gta aaa ctg ggt ttg aag aag gat	1929
Ile Asn Arg Asn Ala Asp Glu Arg Val Lys Leu Gly Leu Lys Lys Asp	
535 540 545	
gca ttg gaa agc agc aag gac aag ctc aat gag ata gtt aat gag cat	1977
Ala Leu Glu Ser Ser Lys Asp Lys Leu Asn Glu Ile Val Asn Glu His	
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aag gat aaa atc aaa aag gta ctt agg ggg agg aat cct ttt gag aag	2025
Lys Asp Lys Ile Lys Lys Val Leu Arg Gly Arg Asn Pro Phe Glu Lys	
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gat atg aag aag gag atc aat caa gcc ttt tgg cct gtg gac aag gaa	2073
Asp Met Lys Lys Glu Ile Asn Gln Ala Phe Trp Pro Val Asp Lys Glu	
580 585 590	
tac aat gag tta aga tca aaa tcc cag gaa gca gag caa gag ctt aaa	2121
Tyr Asn Glu Leu Arg Ser Lys Ser Gln Glu Ala Glu Gln Glu Leu Lys	

00622ED" 96E8E560

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Phe Thr Gln Ser Lys Val Thr Asp Ala Arg Glu Gln Leu Thr Lys Leu	615	620	625	
cga aga gat atg gat gca aaa aga aga ttc ctg gac tcg aaa ctt caa				2217
Arg Arg Asp Met Asp Ala Lys Arg Arg Phe Leu Asp Ser Lys Leu Gln	630	635	640	
tct att tta cag ata tct gct aat gtt gac atg ttt ccc aaa gtt cta				2265
Ser Ile Leu Gln Ile Ser Ala Asn Val Asp Met Phe Pro Lys Val Leu	645	650	655	
caa gac gcc atg aac aaa aga gat gaa cag aaa aga tta gag aat ttc				2313
Gln Asp Ala Met Asn Lys Arg Asp Glu Gln Lys Arg Leu Glu Asn Phe	660	665	670	
gca aat gga atg cgg gaa atg ctt gca cct ttt gaa cat ttg gct cgg				2361
Ala Asn Gly Met Arg Glu Met Leu Ala Pro Phe Glu His Leu Ala Arg	675	680	685	690
aag aat cat gta tgc cca tgc tgt gaa cgt gct ttc aca cct gat gag				2409
Lys Asn His Val Tys Pro Cys Cys Glu Arg Ala Phe Thr Pro Asp Glu	695	700	705	
gag gat gag ttc gtg aag aaa caa agg atg caa aac tca agt act gca				2457
Glu Asp Glu Phe Val Lys Lys Gln Arg Met Gln Asn Ser Ser Thr Ala	710	715	720	
gag aga tct aaa gct ctg gca atg gaa tca tca aat gct gaa gct ctt				2505
Glu Arg Ser Lys Ala Leu Ala Met Glu Ser Ser Asn Ala Glu Ala Leu	725	730	735	
ttt cag caa ttg gat aaa ctt cgg act atc tat gat gct tat gtg aag				2553
Phe Gln Gln Leu Asp Lys Leu Arg Thr Ile Tyr Asp Ala Tyr Val Lys	740	745	750	
ctg gta gaa gaa acc ata cct cta gca gag aaa aac ttg aat caa cat				2601
Leu Val Glu Glu Thr Ile Pro Leu Ala Glu Lys Asn Leu Asn Gln His	755	760	765	770
ttg gcg gat gaa agt cag aag gcg cag gca ttt gat gat ctt ttg ggt				2649
Leu Ala Asp Glu Ser Gln Lys Ala Gln Ala Phe Asp Asp Leu Leu Gly	775	780	785	
gtt ctt gcc cat gtt caa atg gac agg gat gca gtg gaa gcc tta tta				2697
Val Leu Ala His Val Gln Met Asp Arg Asp Ala Val Glu Ala Leu Leu	790	795	800	
caa ccc act gat act att gac agg cat gta cat gaa att caa cag cta				2745
Gln Pro Thr Asp Thr Ile Asp Arg His Val His Glu Ile Gln Gln Leu	805	810	815	
gtc aaa gaa gta gaa gat ctt gaa tat gca ctt gat tct agt ggc cga				2793
Val Lys Glu Val Glu Asp Leu Glu Tyr Ala Leu Asp Ser Ser Gly Arg	820	825	830	
ggt gtc aag tct ttg gag gaa att caa ctg gag ctg aac ttt ctg cag				2841
Gly Val Lys Ser Leu Glu Glu Ile Gln Leu Glu Leu Asn Phe Leu Gln	835	840	845	850

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cat aga atg cta aat gaa gat atg tca agt gct cag gtg aga tgg cac	2937
His Arg Met Leu Asn Glu Asp Met Ser Ser Ala Gln Val Arg Trp His	
870 875 880	
aat gct cgg gaa gag aaa gtg aaa gct tct agc ata ttg gaa aga ttc	2985
Asn Ala Arg Glu Glu Lys Val Lys Ala Ser Ser Ile Leu Glu Arg Phe	
885 890 895	
caa aaa tct gaa gag gaa ttg gtg ctt cta gct gag gaa aaa gaa caa	3033
Gln Lys Ser Glu Glu Glu Leu Val Leu Leu Ala Glu Glu Lys Glu Gln	
900 905 910	
ctg att gta gaa aag aag ctt tta gaa gag tct ctt gat cca ttg tcc	3081
Leu Ile Val Glu Lys Lys Leu Leu Glu Glu Ser Leu Asp Pro Leu Ser	
915 920 925 930	
aaa gag aaa gag agc ttg ttg caa gag tat aat gct ttg aag caa aag	3129
Lys Glu Lys Glu Ser Leu Leu Gln Glu Tyr Asn Ala Leu Lys Gln Lys	
935 940 945	
ctg gat gaa gag tat cat cag ctt gca gaa aga aaa agg gag ttc cag	3177
Leu Asp Glu Glu Tyr His Gln Leu Ala Glu Arg Lys Arg Glu Phe Gln	
950 955 960	
caa gaa ctt gat gct ctt gga aga ctt aat atg aag ata aaa ggg tac	3225
Gln Glu Leu Asp Ala Leu Gly Arg Leu Asn Met Lys Ile Lys Gly Tyr	
965 970 975	
ttg gat tcc aag aaa aac gaa aag ctt aag gaa ttg cag gga agg cat	3273
Leu Asp Ser Lys Lys Asn Glu Lys Leu Lys Glu Leu Gln Gly Arg His	
980 985 990	
gtt ctt tgc cat tct cag tta cag agt tgc atg gca aaa cag caa aga	3321
Val Leu Cys His Ser Gln Leu Gln Ser Cys Met Ala Lys Gln Gln Arg	
995 1000 1005 1010	
ata tca gct gag tta aac aag agc aaa gaa cta ctg cag ggc cag ggc	3369
Ile Ser Ala Glu Leu Asn Lys Ser Lys Glu Leu Gln Gly Gln Gly	
1015 1020 1025	
cag ttg aaa aga aac att gat gac aat ctc aag tac agg aaa aca aag	3417
Gln Leu Lys Arg Asn Ile Asp Asp Asn Leu Lys Tyr Arg Lys Thr Lys	
1030 1035 1040	
gct gat gtg gaa caa ctt act cgt gat ata gaa tca ctt gaa gaa agg	3465
Ala Asp Val Glu Gln Leu Thr Arg Asp Ile Glu Ser Leu Glu Glu Arg	
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ctg ctt tca ata ggt agc ttg tct gct ata gaa gct gat ctg aaa cgc	3513
Leu Leu Ser Ile Gly Ser Leu Ser Ala Ile Glu Ala Asp Leu Lys Arg	
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cat tct caa gaa aaa gag agg ctt aat tca gaa ttt aac agg tgg caa	3561
His Ser Gln Glu Lys Glu Arg Leu Asn Ser Glu Phe Asn Arg Trp Gln	
1075 1080 1085 1090	
gga aca ctt tct gtt tat caa agt aat att tca aag cac aaa caa gag	3609
Gly Thr Leu Ser Val Tyr Gln Ser Asn Ile Ser Lys His Lys Gln Glu	

006220" 968360

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Phe Leu Gln Leu Lys Thr Thr Glu Met Ala Asn Lys Asp Leu Asp Arg			
1125	1130	1135	
tat tat act gct tta gac aag gct ctt atg cgg ttc cac agc atg aag			3753
Tyr Tyr Thr Ala Leu Asp Lys Ala Leu Met Arg Phe His Ser Met Lys			
1140	1145	1150	
atg gag gag ata aat aaa ata atc aag gaa ctg tgg caa cag aca tac			3801
Met Glu Glu Ile Asn Lys Ile Ile Lys Glu Leu Trp Gln Gln Thr Tyr			
1155	1160	1165	1170
aga ggc cag gat att gat tac ata agc ata aat tct gat tct gag ggt			3849
Arg Gly Gln Asp Ile Asp Tyr Ile Ser Ile Asn Ser Asp Ser Glu Gly			
1175	1180	1185	
gct ggc act cga tca tac agc tac cgc gtt gtt atg caa act ggt gat			3897
Ala Gly Thr Arg Ser Tyr Ser Tyr Arg Val Val Met Gln Thr Gly Asp			
1190	1195	1200	
gct gag ctg gaa atg cga ggg cgc tgc agt gct ggt cag aag gtt ctt			3945
Ala Glu Leu Glu Met Arg Gly Arg Cys Ser Ala Gly Gln Lys Val Leu			
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gct tct ctt ata atc aga cta gca ctt gcg gaa act ttc tgc ctg aac			3993
Ala Ser Leu Ile Ile Arg Leu Ala Leu Ala Glu Thr Phe Cys Leu Asn			
1220	1225	1230	
tgc ggt ata ttg gct ttg gat gag cca act acg aat cta gat ggg cca			4041
Cys Gly Ile Leu Ala Leu Asp Glu Pro Thr Thr Asn Leu Asp Gly Pro			
1235	1240	1245	1250
aat gca gag agt ctt gct gct gcg ctg ttg aga ata atg gaa gcc agg			4089
Asn Ala Glu Ser Leu Ala Ala Ala Leu Leu Arg Ile Met Glu Ala Arg			
1255	1260	1265	
aaa ggg cag gag aac ttc cag ttg att gta atc act cat gat gag aga			4137
Lys Gly Gln Glu Asn Phe Gln Leu Ile Val Ile Thr His Asp Glu Arg			
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ttt gcc cat ctt atc ggt caa agg cag ctt gct gag aag tac tat cga			4185
Phe Ala His Leu Ile Gly Gln Arg Gln Leu Ala Glu Lys Tyr Tyr Arg			
1285	1290	1295	
gtc tcc aag gat gag aac cag cac agc ata att gaa tcc caa gag ata			4233
Val Ser Lys Asp Glu Asn Gln His Ser Ile Ile Glu Ser Gln Glu Ile			
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Phe Asp			
1315			
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gccagaggat ggaatgtgtg cactgggtga tggatgtttc acgacatcaa tgaatgtttc			4469
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Val	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Thr	Thr	Ile	Ile	Glu	Cys	Leu	Lys
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Phe	Val	His	Asp	Pro	Lys	Val	Ala	Gly	Glu	Thr	Glu	Thr	Lys	Gly	Gln
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Ile	Lys	Leu	Arg	Phe	Lys	Thr	Ala	Ala	Gly	Lys	Asp	Val	Val	Cys	Ile
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Arg	Ser	Phe	Gln	Leu	Thr	Gln	Lys	Ala	Ser	Lys	Met	Glu	Phe	Lys	Ala
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Cys	Leu	Ser	Tyr	Arg	Cys	Ala	Asp	Met	Asp	Arg	Glu	Ile	Pro	Ala	Leu
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Met	Gly	Val	Ser	Lys	Ala	Val	Leu	Glu	Asn	Val	Ile	Phe	Val	His	Gln
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Asp	Glu	Ser	Asn	Trp	Pro	Leu	Gln	Asp	Pro	Ser	Thr	Leu	Lys	Lys	Lys
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Phe	Asp	Asp	Ile	Phe	Ser	Ala	Thr	Arg	Tyr	Thr	Lys	Ala	Leu	Glu	Val
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Ile	Lys	Lys	Leu	His	Lys	Asp	Gln	Met	Gln	Glu	Ile	Lys	Thr	Phe	Arg
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Leu	Lys	Leu	Glu	Asn	Leu	Gln	Thr	Val	Lys	Asp	Gln	Ala	His	Lys	Leu
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Arg	Glu	Asn	Ile	Ala	Gln	Asp	Gln	Glu	Lys	Ser	Asp	Ala	Ser	Lys	Ser
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Gln	Met	Glu	Gln	Leu	Lys	Glu	Lys	Ile	Cys	Gly	Thr	Glu	Arg	Glu	Ile
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Leu	Gln	Met	Glu	Thr	Ser	Leu	Asp	Glu	Leu	Arg	Arg	Leu	Gln	Gly	Gln
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Glu	Lys	Leu	Ala	Ala	Leu	Ser	Glu	Glu	Asn	Glu	Asp	Thr	Asp	Glu	Glu
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Leu	Met	Glu	Trp	Gln	Thr	Lys	Phe	Glu	Glu	Arg	Ile	Ala	Leu	Leu	Glu
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Thr	Lys	Ile	Ser	Lys	Leu	Val	Arg	Asp	Met	Asp	Asp	Glu	Ala	Ser	Tyr
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Ser	Ser	Val	Leu	Ser	Lys	Gln	Asn	Ser	Glu	Leu	Thr	His	Glu	Ile	Gly
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Asp	Ser	Asp	Ile	Lys	Asn	Ile	Cys	Thr	Lys	His	Asn	Leu	Gly	Pro	Val
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Pro	Glu	His	Pro	Phe	Thr	Asn	Asp	Val	Ala	Met	Asn	Leu	Thr	Asn	Arg
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Lys	Ser	Asn	Glu	Asp	Gln	Leu	Asp	Val	Leu	Trp	Lys	His	Tyr	Leu	Lys
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Ile	Asn	Ala	Arg	Tyr	Ser	Glu	Val	Asp	Gly	Gln	Ile	Gln	Ser	Lys	Ile

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Arg	Asp	Ala	Ala	Glu	Val	Glu	Leu	Ser	Lys	Phe	Asn	Leu	Ser	Arg	Ile			
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Glu	Val	Tyr	Ser	Leu	Glu	Gln	Lys	Ile	Lys	Val	Leu	Leu	Arg	Glu	Lys			
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Lys	Asp	Ala	Leu	Glu	Ser	Ser	Lys	Asp	Lys	Leu	Asn	Glu	Ile	Val	Asn			
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Leu	Gln	Ser	Ile	Leu	Gln	Ile	Ser	Ala	Asn	Val	Asp	Met	Phe	Pro	Lys			
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Ala	Arg	Lys	Asn	His	Val	Cys	Pro	Cys	Cys	Glu	Arg	Ala	Phe	Thr	Pro			
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Asp	Glu	Glu	Asp	Glu	Phe	Val	Lys	Lys	Gln	Arg	Met	Gln	Asn	Ser	Ser			
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Thr	Ala	Glu	Arg	Ser	Lys	Ala	Leu	Ala	Met	Glu	Ser	Ser	Asn	Ala	Glu			
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Ala	Leu	Phe	Gln	Gln	Leu	Asp	Lys	Leu	Arg	Thr	Ile	Tyr	Asp	Ala	Tyr			
			740					745					750					
Val	Lys	Leu	Val	Glu	Glu	Thr	Ile	Pro	Leu	Ala	Glu	Lys	Asn	Leu	Asn			
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Gln	His	Leu	Ala	Asp	Glu	Ser	Gln	Lys	Ala	Gln	Ala	Phe	Asp	Asp	Leu			
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 Phe Gln Gln Glu Leu Asp Ala Leu Gly Arg Leu Asn Met Lys Ile Lys
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 980 985 990
 Arg His Val Leu Cys His Ser Gln Leu Gln Ser Cys Met Ala Lys Gln
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 Glu Ile Phe Asp
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 used for cDNA library construction and poly(dT) to
 remove clones which have a poly(A) tail but no
 cDNA insert.

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36

0052E0" 96E8E560